

Db 170 RRRVEIALDLTERQVKWFQNRHMKHKTQTHREPPDEBPACGALIEDICDPAEBA 229
 QY 133 LSRGISDAPAPW-----PP-----PG-----DPPGTPPG 158
 Db 230 ASPGSPASRAAMWACCHPEVVPGALSDPRPLAVRLGAGASSPG 276

RESULT 9

albumin D-box binding protein - human
 A:Accession: A55558
 C:Species: Homo sapiens (man)
 C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 01-Dec-2000
 C:Accession: A55558; G02887
 R:Khatib, Z. A.; Inaba, T.; Valentine, M.; Look, A. T.
 Genomics 23, 344-351, 1994
 A>Title: Chromosomal localization and cDNA cloning of the human DBP and TEF genes.
 A:Reference number: A55558; MUID:95137580; PMID:7835883
 A:Accession: A55558
 A:Status: preliminary
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-335 <KHA>
 A:Cross-references: GB:U06936; NID:9606798; PIDN:AAA81374.1; PID:9606799
 R:Mueller, C. R.
 submitted to the EMBL Data Library, February 1996
 A:Reference number: H01797
 A:Accession: G02887
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-178, 'S', 180-325 <KUE>
 A:Cross-references: EMBL:U48213; NID:g1208753; PID:g1208754
 C:Accession:
 A:Gene: GDB:DBP
 A:Cross-references: GDB:128840; OMIM:124097
 A:Map position: 4q12-4q12
 A:Introns: 47/1; 184/1; 254/3

Query Match 11.0%; Score 106; DB 2; Length 325;
 Best Local Similarity 26.6%; Pred. No. 0.81;
 Matches 55; Conservative 13; Mismatches 77; Indels 62; Gaps 9;

QY 4 GPRSLRGDAPAPTPCVPA-----ECFPL---LVHCVACGLLTPPKXAG 47
 Db 83 GGGSPGRGPPAPPLALPLMERTLPFGDVEYVDLDFLLEH-----GL--PPSPPPG 136
 QY 48 ASSPARTLOQESVAGAGGALP--LPGLFGAPALLGLALVLAIVLVGIVSMRRQ 105
 Db 137 GSPSPSPARTPSPGSGSASPRSSPG--HAPAPALGT----- 177
 QY 106 RRLGASSAEPDGDKADPEPLDKVILSPGISDATAPAMPPEGDPGTPPGHSVPVA 165
 Db 178 -----ATGHRAGLTSDTSPVD-----PDTEVLTPEPPADLALSIQHETFDPR 226
 QY 166 TELGSTELV-----TTKTAGEEQ 184
 Db 227 RHRFSEELKQPIPMKKARKIQVEEQ 253

RESULT 10

Basoon protein - rat
 N:Alternate names: brain-specific synapse-associated protein
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
 C:Accession: T42761
 R:Dieck, S.; Sammarti-Vila, L.; Langnaese, K.; Richter, K.; Kindler, S.; Soyke, A.; Wex, J. Cell Biol. 142, 499-509, 1998
 A>Title: Basoon, a novel zinc-finger CAG/Glutamine-repeat protein selectively localized
 A:Reference number: 222242; MUID:98345363; PMID:9679147
 A:Accession: T42761
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-3938 <DIE>
 A:Cross-references: EMBL:Y16563; NID:g3413503; PIDN:CAA76287.1; PID:g3413504

A:Experimental source: strain Sprague Dawley; brain
 C:Function:
 A:Description: may be involved in cytoskeletal organization at the site of neurotransmitter
 A>Note: component of the presynaptic cytoskeleton
 C:Keywords: coiled coil; zinc finger

Query Match 10.8%; Score 104.5; DB 2; Length 3938;
 Best Local Similarity 26.8%; Pred. No. 1.1;
 Matches 53; Conservative 13; Mismatches 73; Indels 59; Gaps 10;

QY 4 GPR---SLRGDAPAPTPC-VPACFDLLVHCVACGLLTPPKPAGASAPPTALOP 59
 Db 272 GPRQEAARAPATSVPGPTATAPPE-----VGRVSPQPPSLSTKPSA--EP 314
 QY 60 QESVGAGGALP-----GLFGAPALLGLALVLAIVLVGIVSMRRQ 105
 Db 315 RPPAEAGSKATVTPSGLAABQTGGTGLTFLGLASL--LTQASTLISVQP----- 366
 QY 106 RRLGASSAEPDGDKADPEPLDKVILSPGISDATAPAMPPE--GPDGTPPGHSVP 162
 Db 367 ----EADTGGQSPSPKPP---KIV-----FSDASKKAGRPSPGSGPPTPGAKTEP 413
 QY 163 VPATELGSTELVTTKTAG 180
 Db 414 GPRTPGSGPGALAKTGG 431

RESULT 11

gene Lf3 protein - human herpesvirus 4
 C:Species: human herpesvirus 4, Epstein-Barr virus
 C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Jan-2000
 C:Accession: S27923
 R:Parker, B. D.; Bankier, A.; Satchwell, S.; Barrel, B.; Farrell, P. J.
 submitted to the EMBL Data Library, August 1990
 A:Description: Sequence and transcription of Raji Epstein-Barr virus DNA spanning the B9
 A:Reference number: S27923
 A:Accession: S27923
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-924 <PAR>
 A:Cross-references: EMBL:M35547; NID:g330420; PIDN:AAA45896.1; PID:g330421
 C:Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;

Query Match 10.7%; Score 103.5; DB 2; Length 924;
 Best Local Similarity 28.6%; Pred. No. 3.3;
 Matches 54; Conservative 14; Mismatches 68; Indels 53; Gaps 9;

QY 32 CVA--CGLLTPRPAPAGASSPA-----PTALQPOESVAGAGGALPL 74
 Db 9 CLAPSGGAGHPRRSAGADPADPVGHAPAPAGPPTRLQATPRRSAGADPADPV 68
 QY 75 PGLLGAPALLGLALVLAIVLVGIVSMRRQ--RRLGASSAEPDGDKDA----PEP 126
 Db 69 -----GHPA-----APRAGPEPRTRLQATPRRSAGADPADPVGHAPAPAGPBP 115
 QY 127 LDKVILSPGISDATAPAMP-----PGSDPT-----TPPGHSVPVATELGSTEL 173
 Db 116 RTRLPATPRRSAGADPADPVGHAPAPAGPPEPRTRLQATPRRSAGADPADPVGH 173
 QY 174 VTTKTAGEP 182
 Db 174 AAPRAGPBP 182

RESULT 12

actin-depolymerizing protein N-WASP, brain - bovine
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 23-Apr-1998 #sequence_revision 01-May-1998 #text_change 05-Nov-1999
 C:Accession: S72273
 R:Miki, H.; Mura, K.; Takenawa, T.
 EMBO J. 15, 5326-5335, 1996

A:Title: N-WASP, a novel actin-depolymerizing protein, regulates the cortical cytoskeleton
 A:Reference number: S72273; MUID:97050838; PMID:8895577
 A:Accession: S72273
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-505 <MIR>
 A:Cross-references: EMBL:D67066; NID:g1644231; PIDN:BA11082.1; PID:dl011742; PID:g16442
 A:Experimental source: brain

Query Match 10.7%; Score 103; DB 2; Length 505;
 Best Local Similarity 23.6%; Pred. No. 2;
 Matches 41; Conservative 4; Mismatches 45; Indels 84; Gaps 7;

QY 5 PSLGRDAPAPTPC-VPAECFDLVRHCACGLLRTPPKPA---GASSAPATLAP 59
 DB 301 PPPAGRGAPPPPSAPPTA-----PPPPPSREGVAPPPPPNMP 345
 QY 60 QESVAGAGEALPLPGLLFGAPALLGLALVTLVGLVSWRRORRLGASSAPAPDG 119
 DB 346 -----PLPAL-----PSSAPSG 357
 120 DKDAPEPLDKVIIISPGISDATAPAMPPEGDEPTTP-----GHSVPYPA 165
 DB 358 PPPPPPL-----SVSGVAPPPPPPPPPPPGGLPSDGDHQPPTPA 403

RESULT 13

hypothetical protein SPAC23A1.17 - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C:Accession: T38236
 R:Murphy, L.; Harris, D.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, February 1998
 A:Reference number: Z21780
 A:Accession: T38236
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1611 <MUR>
 A:Cross-references: EMBL:AL021813; PIDN:CA16991.1; GSPDB:GN00066; SPDB:SPAC23A1.17
 A:Experimental source: strain 972h-, cosmid c23A1
 A:Genetics:
 A:Gene: SPDB:SPAC23A1.17
 A:Map position: 1

Query Match 10.7%; Score 103; DB 2; Length 1611;
 Best Local Similarity 24.6%; Pred. No. 6;
 Matches 44; Conservative 16; Mismatches 71; Indels 48; Gaps 7;

DB 13 AAPTPCVPAEAGFDLVRHCACGLLRTPPKPAAGASSAPATLAPQESVAGAGEAL 72
 DB 1078 AASGAPVPA-----PSGITPPVVKPSVAPVVKPSVAVP---VAPASGAPV 1123
 QY 73 PLPGLL-----FGAPALLGLALVTLVGLVSWRRORRLGASSAPAPDGDAPE 125
 DB 1124 PKPSVAPAPVVPVPSGAPV-----PKPSVAPAPVAPASG---AP- 1159
 QY 126 PLDKVIIISPGI---SDAPAPAMPPEGDEPTTPPGHSVVPATLGLSTELVTTKAGP 161
 DB 1160 PVPKSVAPAPVAPASGIGIPVVKPAPAGVVPVPPSEAPVVKPSVGVVPPPPSTAPP 1218

RESULT 14

hypothetical protein 15E6.220 [imported] - Neurospora crassa
 C:Species: Neurospora crassa
 C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-May-2000
 C:Accession: T48814
 R:Schulte, U.; Aism, V.; Hohnselt, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
 submitted to the Protein Sequence Database, April 2000
 A:Reference number: Z24541
 A:Accession: T48814
 A:Status: preliminary

A:Molecule type: DNA
 A:Residues: 1-1952 <SCH>
 A:Cross-references: EMBL:AL353822; GSPDB:GN00112; NCSP:15E6.220
 A:Experimental source: cosmid contig 15E6, strain 74
 A:Genetics: NCSP:15E6.220
 A:Gene: NCSP:15E6.220
 A:Map position: 2
 A:Introns: 281/3

Query Match 10.7%; Score 103; DB 2; Length 1952;
 Best Local Similarity 29.0%; Pred. No. 7.2;
 Matches 38; Conservative 15; Mismatches 62; Indels 16; Gaps 4;

QY 41 PPPKPAAGSSAPATLAPQESVAGAGEALPLPGLLFGAPALLGLALVTLVGLV 99
 DB 1812 PAPSAAQSVAPVPSSTVPAATVAPASTVAAAPPTVTAPALASATNPAPV----- 1867
 QY 100 SWRRORRLGASSAPADPDGDAPEPLDKVIIIS-----PEISDATAPAMPPEGDEPT 154
 DB 1868 --SQPHOITGQAPAQOQRPAPAOAPATPTTSAAPRPPTLAPPPPPPPTEDPPP 1925
 QY 155 TPFGHSVPYPA 165
 DB 1926 PPP-----PPPA 1932

RESULT 15

legum protein 64 - equine herpesvirus 2
 C:Species: equine herpesvirus 2
 C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 08-Oct-1999
 C:Accession: S55659
 R:Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
 J. Mol. Biol. 249, 520-528, 1995
 A:Title: The DNA sequence of equine herpesvirus 2.
 A:Reference number: S55594; MUID:95302501; PMID:7783207
 A:Accession: S55659
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-3436 <TEL>
 A:Cross-references: GB:U020824; NID:g695172; PIDN:AACT13852.1; PID:g695237
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1995

Query Match 10.7%; Score 103; DB 2; Length 3436;
 Best Local Similarity 25.0%; Pred. No. 12;
 Matches 55; Conservative 12; Mismatches 51; Indels 102; Gaps 11;

QY 2 RRGPSRLGRD-----APAPT-----PCVPAECFDL-----VRHCYAC 35
 DB 3178 RLGERGRERREVEVAADAPRDYRNRPVPRRPGSGRSPARDDTLGGAGSREKVS 3237
 QY 36 G-----LLRTPPKPAAGASSAPATLAPQESVAGAGEALPLPGLLFGAPALLGLA 88
 DB 3238 GGRPRVOLSRSPKPRPAPASQVQGR-----EEVGFSPGRAR----- 3274
 QY 89 LVLALVGLVSWRRORRLGASSAPADPDGDAPEPLDKVIIIS----- 135
 DB 3275 -----KGGSTAHAP-----PE-TTADVTEPRKSGVAGSGEPE 3307
 QY 136 -----GISDATAPAMPPEGDEPTTPPGHSVVPATLGLST 171
 DB 3308 KKQGAABAEAPV-PREGGAAGAPGEGTPEPAS-IGKT 3345

Search completed: June 23, 2003, 15:16:43
 Job time : 49 secs

THIS PAGE BLANK (USPTO)